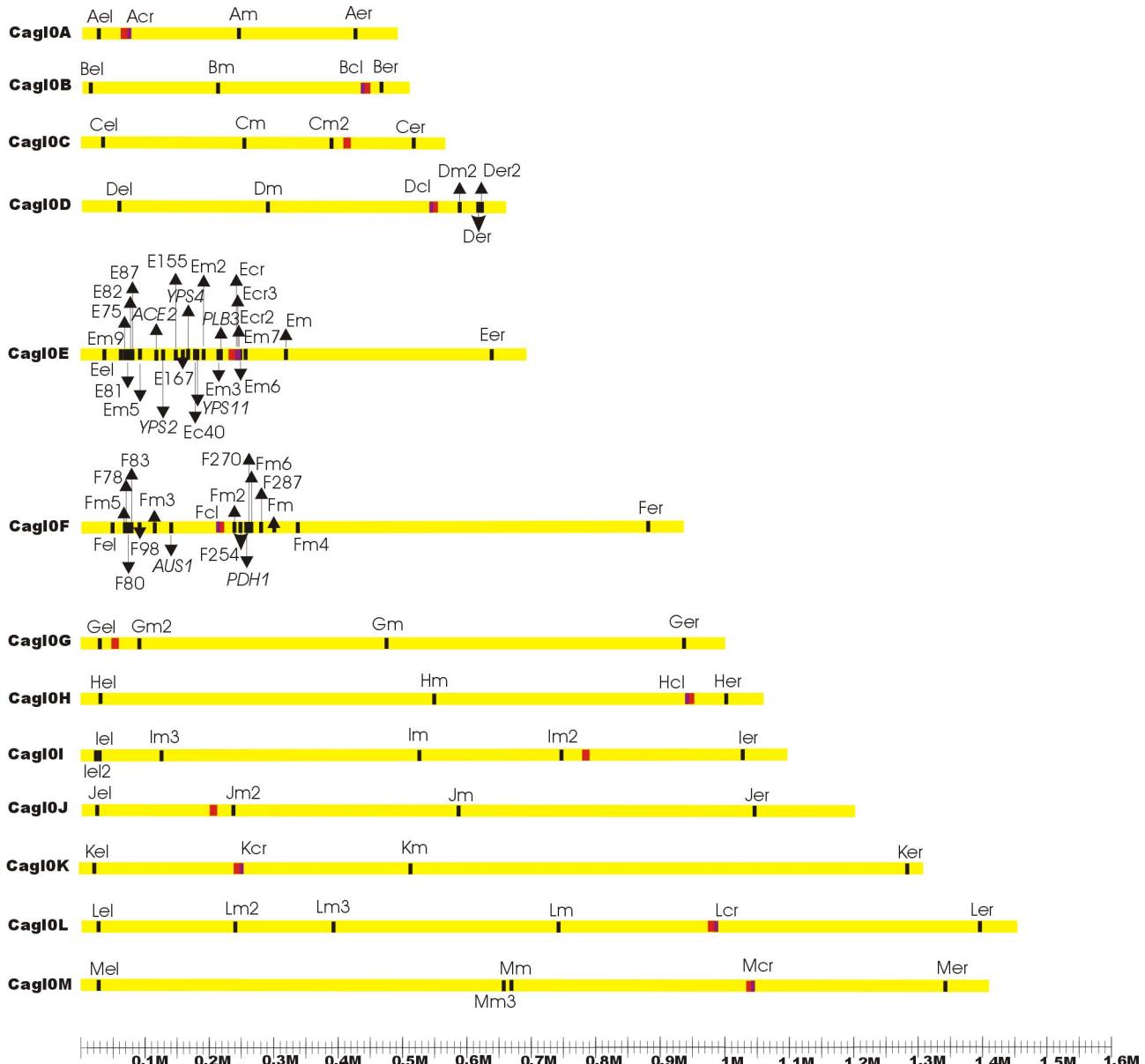
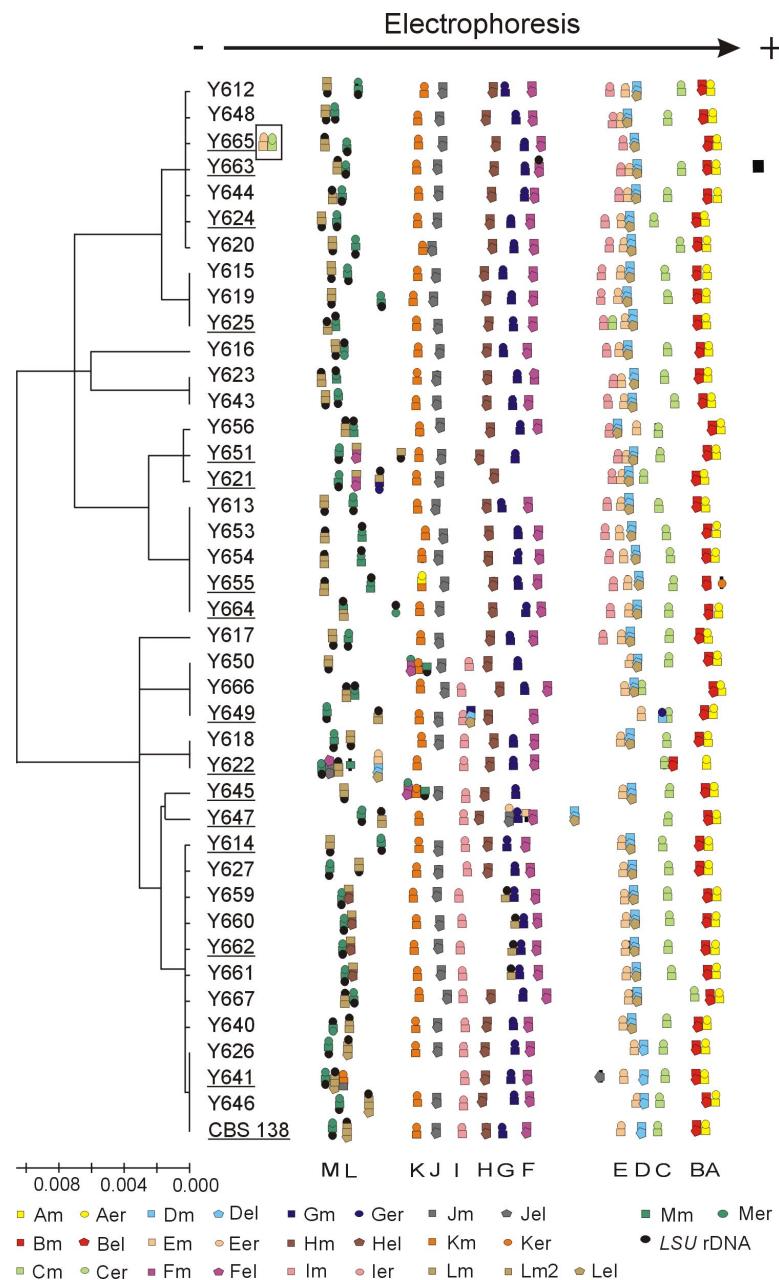


# Supporting Information

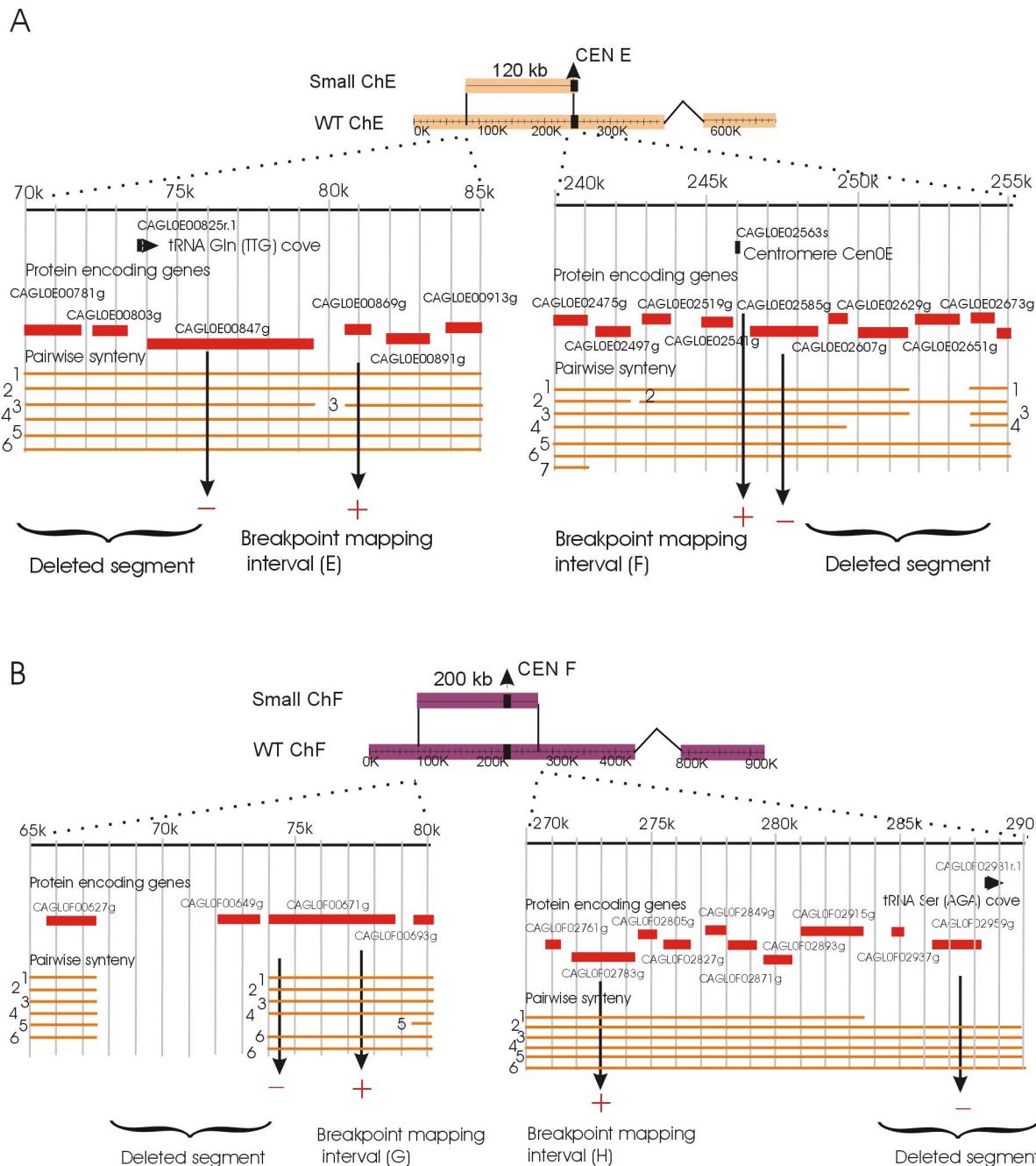
Poláková et al. 10.1073/pnas.0809793106



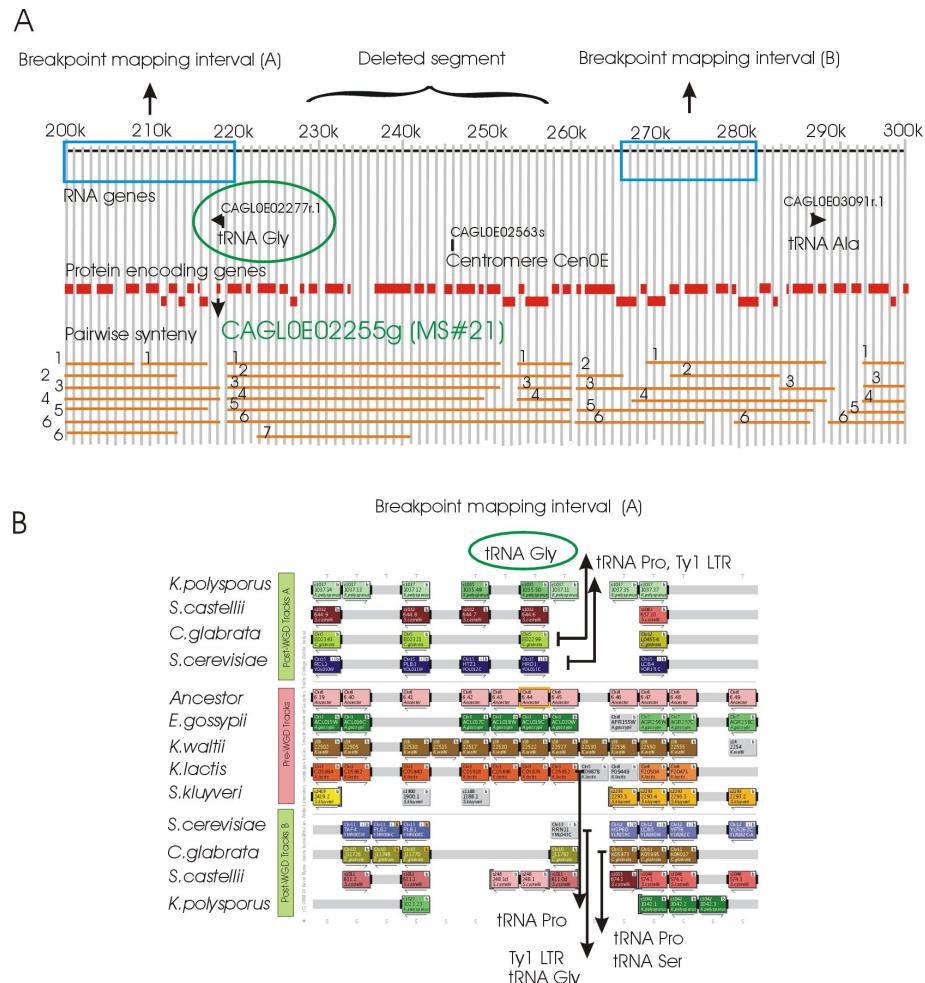
**Fig. S1.** The *C. glabrata* CBS 138 chromosomes with the position of the probes (see also Table S3) used in the Southern blot analysis. Chromosomes are marked from A to M according to the *C. glabrata* nomenclature. Red stripes symbolize the positions of centromeres.



**Fig. S2.** Electrophoretic karyotypes and initial mapping of *C. glabrata* clinical isolates. The phylogenetic relationship is based on the IGS region between the nuclear genes CAGLOA00605g and CAGLOA00627g on chromosome A, and the scale bars represent the number of base substitutions per site. Chromosomes of the sequenced strain CBS 138 are marked from A to M. Two unique probes labeled with the same color were used per chromosome: one from middle of the chromosome marked by squares and one from near the chromosome end, the left end marked as pentagons, and right end marked as circles (see also Fig. S1). Additional probe Lm2 was used to map the left end of chromosome L, because LeL probe in the majority of isolates hybridized to chromosome D. One extra multigene probe hybridizing to *LSU rDNA* gene is illustrated as a black dot. In strain Y665, marked by a black square, probes Em, Eer, Cm and Cer hybridized to the loading well. The underlined strains, covering chromosome changes of all strains, were analyzed in more detail, and the results are presented in Fig. 1. For example, Y659, Y660, Y662, and Y661 exhibit the same translocations and therefore only one strain, Y662, was selected for further mapping.



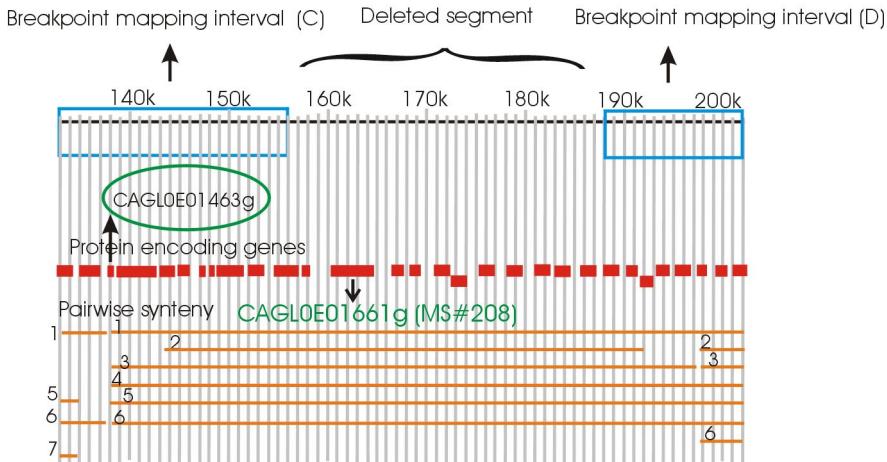
**Fig. S3.** Mapping of the terminal deletions end points. (A) Y624 carries a duplication of chromosome E (Small ChE) corresponding to a ~120-kb fragment (Fig. 3A). WT stands for CBS 138 chromosome architecture. The figure further illustrates a part of original *C. glabrata* chromosome E. The last sequences identified as present on the novel chromosome are marked by vertical arrow and red (+); the first sequences identified as missing by vertical arrow and red (−). For other details see Fig. S4. Within the breakpoint interval (F), the fragile site could be associated with a centromere sequence. (B) Y663 carries a duplication of chromosome F (Small ChF) corresponding to ~200-kb fragment (Fig. 3B). WT stands for CBS 138 chromosome architecture. The figure further illustrates a part of original *C. glabrata* chromosome F.



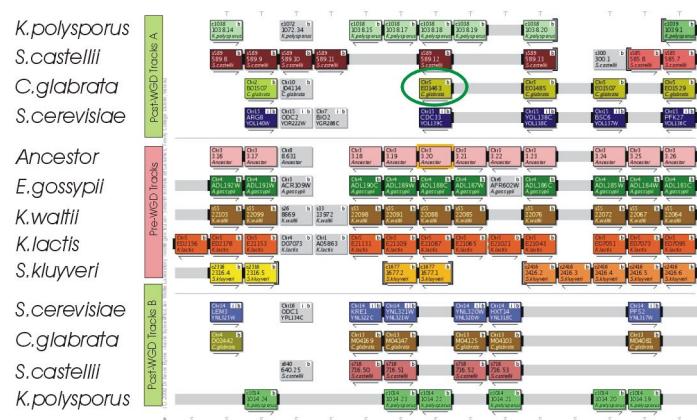
**Fig. S4.** Mapping of the internal deletions end points. (A) The deleted segment of chromosome D+E from Y622 (see also Fig. 3C) encompasses a fragment of 50–80 kb, also covering the centromere E region. The figure illustrates a part of the original *C. glabrata* chromosome E and the blue squares mark the breakpoint mapping intervals. Red boxes denote the positions of the protein coding genes. The gene (CAGLOE02255g) containing a minisatellite (MS#21) (6) is indicated by an arrow and is colored in green and maps relatively close to the breakpoint. Pairwise syntenic blocks (illustrated by orange lines) in Hemiascomycete yeasts (1. *Eremothecium gossypii*, 2. *Kluyveromyces lactis*, 3. *Kluyveromyces thermotolerans*, 4. *Saccharomyces kluyveri*, 5. *Zygosaccharomyces rouxii*, 6. *Saccharomyces cerevisiae*, 7. *C. glabrata*) were obtained by i-ADHoRE method (1) using the Génolevures database and genome sequences determined by the Génolevures Consortium (2). Note that *S. cerevisiae* and *C. glabrata* are post-WGD species and therefore two syntenic regions can be found. The orange lines are interrupted when the gene order of the analyzed *C. glabrata* segment is no longer collinear with the gene order of the homologous segments from Hemiascomycete yeasts. The breakpoint interval (A) containing the tRNA genes and a minisatellite (MS#21) (3) seems to be prone to rearrangements. (B) The breakpoint interval (A) within the chromosome D+E from Y622 coinciding with “historical” breakpoints. The figure additionally illustrates synteny relationships within and between the genomes of seven Hemiascomycete yeasts (post-WGD species: *S. cerevisiae*, *C. glabrata*, *Saccharomyces castellii*, and *Kluyveromyces polyporus* and pre-WGD species: *E. gossypii*, *K. lactis*, *S. kluyveri*, hypothetical ancestor), which were obtained by the Yeast Gene Order Browser (YGOB) (4). The *S. castellii*, *K. polyporus*, and *S. kluyveri* genomes are annotated in contigs, and the genomes of other yeasts are assembled into chromosomes. Each box illustrates a gene and each color illustrates a chromosome. Nonsyntenic genes are colored in gray. The analyzed gene is marked by a green circle. The gene, which was used to compose the entire display is marked by an orange border. Genes are joined by a solid bar for adjacent genes. The end of the chromosome or a contig is marked by a brace. Horizontal arrows illustrate relative transcriptional orientation. The position of tRNA genes and transposons in yeast genomes is marked by black vertical arrows. At the site associated with tRNA genes the gene order was changed, comparing to hypothetical ancestor, in all analyzed Hemiascomycetes. (C) The deleted segment of the novel chromosome from Y624 (Fig. 3A) encompasses a fragment of 40–60 kb. The figure illustrates a part of the original *C. glabrata* chromosome E and the blue squares mark the breakpoint intervals. In the middle of the internal deletion a megasatellite (MS#208), mapping to CAGLOE01661g (indicated by an arrow and colored in green), is located. (D) The breakpoint interval (C) within the novel chromosome from Y624 coinciding with historical breakpoints. The gene (CAGLOE01463g) is highlighted by a green ellipse. Within the breakpoint interval (C) the yeast genomes often carry nonsyntenic homologs (gray boxes). In addition, the gene order of both *C. glabrata* regions has been changed at this site during the evolutionary history.

- Simillion C, Janssens K, Sterck L, Van de Peer Y (2008) i-ADHoRe 2.0: An improved tool to detect degenerated genomic homology using genomic profiles. *Bioinformatics* 24:127–128.
- Sherman D, et al. (2006) Génolevures complete genomes provide data and tools for comparative genomics of hemiascomycetous yeasts. *Nucleic Acids Res* 34:D432–D435.
- Thierry A, Bouchier C, Dujon B, Richard GF (2008) Megasatellites: a peculiar class of giant minisatellites in genes involved in cell adhesion and pathogenicity in *Candida glabrata*. *Nucleic Acids Res* 36:5970–5982.
- Byrne KP, Wolfe KH (2006) Visualizing synteny relationships among the hemiascomycetes with the Yeast Gene Order Browser. *Nucleic Acids Res* 34:D452–D455.

C



D



**Fig. S4.** Continued.

**Table S1. *C. glabrata* clinical isolates originating from the Danish Statens Serum Institute collection and their in vitro susceptibility to fluconazole**

Strain laboratory designation	Museum number	Year of isolation	Place of isolation	Source	Fluconazole MIC, mg/L
Y612	A264/99	1999	Unknown	Unknown	43.2
Y613	A292/99	1999	Unknown	Unknown	43.2
Y614	OO4101	1996	Bispebjerg	Blood	43.2
Y615	OO4114	1996	Copenhagen-Rigshospitalet	Blood	14.4
Y616	OO4132	1996	Nykøbing Falster	Blood	14.4
Y617	OO4492	1996	Århus	Unknown	43.2
Y618	OO4511	1996	Nykøbing Falster	Blood	43.2
Y619	OO4524	1996	Bispebjerg	Blood	14.4
Y620	OO4534	1996	Bispebjerg	Blood	43.2
Y621	OO4540	1996	Aalborg	Blood	43.2
Y622	OOO117	1986	Copenhagen-Rigshospitalet	Blood	129.6
Y623	OOO119	1986	Roskilde	Blood	388.8
Y624	OOO127	1986	Brændstrup	Blood	43.2
Y625	OOO149	1986	Copenhagen-Rigs	Lymph node	129.6
Y626	OOO179	1986	Herlev	Palate	43.2
Y627	OOO182	1986	Unknown	Blood	129.6
Y640	OO2475	1992	Kolding	Urine	14.4
Y641	OO2516	1992	London	Standard strain	43.2
Y643	OO2561	1992	Copenhagen-Rigshospitalet	Feces	43.2
Y644	OO2574	1992	Copenhagen-Rigshospitalet	Throat	43.2
Y645	OO2576	1992	Copenhagen-Rigshospitalet	Unknown	43.2
Y646	OO2684	1992	Gentofte	Gland	129.6
Y647	OO2699	1992	Copenhagen-Rigshospitalet	Unknown	14.4
Y648	OO2706	1992	Viborg	Blood	14.4
Y649	OO2736	1992	Hvidovre	Catheter spit	43.2
Y650	OO2742	1992	Slagelse	Blood	43.2
Y651	OO2792	1992	Copenhagen-Rigshospitalet	Feces	43.2
Y653	OO2806	1992	Bispebjerg	Blood	43.2
Y654	OO2807	1992	Bispebjerg	Blood	43.2
Y655	OO2808	1992	Bispebjerg	Blood	43.2
Y656	OO2811	1992	Hillerød	Feces	43.2
Y659	OO2864	1992	Køge	Blood	14.4
Y660	OO2865	1992	Køge	Blood	14.4
Y661	OO2866	1992	Køge	Blood	14.4
Y662	OO2867	1992	Køge	Blood	14.4
Y663	OO2870	1992	Copenhagen-Rigshospitalet	Feces	129.6
Y664	OO2889	1992	Copenhagen- Frederiksberg	Blood	43.2
Y665	OO2895	1992	Unknown	Feces	129.6
Y666	OO2899	1992	Copenhagen-Rigshospitalet	Feces	43.2
Y667	OO2901	1992	Århus	Blood	43.2

The year, place (hospital), and tissue source of isolates are listed. In general, these patients received antifungal treatment. Y numbers refer to the Piškur laboratory collection at Lund University. Museum numbers belong to the Danish Statens Serum Institute collection.

**Table S2. Deposited gene sequences of the analyzed clinical isolates of *C. glabrata***

Strain laboratory designation	LSU rDNA GenBank accession no.	mt SSU rDNA GenBank accession no.	IGS (CDH1-ERP6) GenBank accession no.
Y612	AF490139	AF490006	AM982681
Y613	AF490138	AF490007	AM982682
Y614	AF369483	AF490008	AM982683
Y615	AF369484	AF490009	AM982684
Y616	AF369485	AF490010	AM982685
Y617	AF369486	AF490011	AM982686
Y618	AF369487	AF490012	AM982687
Y619	AF369488	AF490013	AM982688
Y620	AF369489	AF490014	AM982689
Y621	AF369490	AF490015	AM982690
Y622	AF369491	AF490016	AM982691
Y623	AF369492	AF490017	AM982692
Y624	AF369493	AF490018	AM982693
Y625	AF369494	AF490019	AM982694
Y626	AF369495	AF490020	AM982695
Y627	AF369496	AF490021	AM982696
Y640	AF369497	AF490022	AM982697
Y641	AF369498	AF490023	AM982698
Y643	AF369500	AF490025	AM982699
Y644	AF369501	AF490026	AM982700
Y645	AF369502	AF490027	AM982701
Y646	AF369503	AF490028	AM982702
Y647	Not determined	AF490029	AM982703
Y648	AF369504	AF490030	AM982704
Y649	AF369505	AF490031	AM982705
Y650	AF369506	AF490032	AM982706
Y651	AF369507	AF490033	AM982707
Y653	AF369509	AF490035	AM982708
Y654	AF369510	AF490036	AM982709
Y655	AF369511	AF490037	AM982710
Y656	AF369512	AF490038	AM982711
Y659	AF369515	AF490041	AM982712
Y660	AF369516	AF490042	AM982713
Y661	AF369517	AF490043	AM982714
Y662	AF369518	AF490044	AM982715
Y663	AF369519	AF490045	AM982716
Y664	AF369520	AF490046	AM982717
Y665	AF369521	AF490047	AM982718
Y666	AF369522	AF490048	AM982719
Y667	AF369523	AF490049	AM982720

**Table S3. Gene-specific PCR primers used for generation of fragments to be used as 93 single-gene probes and 1 multigene probe in Southern analysis of the separated yeast chromosomes**

Probe name	Primer name	Primer (5'-3')	Product size, bp	Chromosome position, bp
Am	A2365g for	GGAGTATATAACACAGGTACGGA	1000	A, 251824 - 252824
	A2365g rev	CGTTGTCAGCTTCAACGTCTTCATC		
Aer	A4455g for	GTAAGCAGTCCACCACCAAGAAAG	1002	A, 432894 - 433896
	A4455g rev	GTGGTCGTGCAATTATAGGAGAC		
Ael	A0363g for	GAACACGTCTGGCTACCCAAAC	1040	A, 34824 - 35863
	A0363g rev	GGTCAGTGTGCTCATACGCAG		
Acr	A00869g for	GGCAACTGGCGTACTCTTAGATT	993	A, 87887 - 88879
	A00869g rev	GCAGGTAATTACAACGCAGGTC		
Bm	B2365g for	CTCATGAACTCTCCATACCAGAATGTG	897	B, 226798 - 227695
	B2365g rev	CAAATAGAGCATTTGTTCAACCTGTG		
Bel	B0330g for	CCAGAGAACAGACTAGCAATCAGATTG	1182	B, 20160 - 21341
	B0330g rev	CTGAGGAGCTGCTATCAAAGTTCTG		
Ber	B4917g for	GATGAGGCTGTTGAGGAATT	946	B, 477995 - 478940
	B4917g rev	CCTCAGTAGAACATAAGCCGACCTG		
Bcl	B04631g for	GACTGGTAACAAAGGTGCTGTCTC	989	B, 447475 - 448463
	B04631g rev	CTTGTGGACTCAAGACAGTTGGC		
Cm	C2607g for	AGAATTCAAAGACCTGCCTGTTACC	990	C, 266163 - 267152
	C2607g rev	GCAACATCTCCCTCAAAGATTAGATCC		
Cm2	C04048g for	GTACTGTGAATGTGGCGATACC	1080	C, 400411 - 401490
	C04048g rev	GTCCTGAGCTCAAGGTTGTGCC		
Cer	C5489g for	CCGACAAAAGAATTGCAAGACAATGTC	1129	C, 528644 - 529747
	C5489g rev	CCAAACACCAGTGGAAAGATAATAATCC		
Cel	C0407g for	GCATCCGTTCTACACACAAGAAG	983	C, 40862 - 41844
	C0407g rev	CTGGCCATGACTCAAGTTCTACG		
Dm	D2838g for	AAGGCTAAAGGTAAAGAAGAATGGTC	1049	D, 297853 - 298901
	D2838g rev	AAAGGACTCAGGTCTATTGTAGCAC		
Dm2	D06314g for	GATGACTTCAACCACACCAGGTG	1059	D, 596328 - 597386
	D06314g rev	CAAGGATCATCTGGGAAAGGCTC		
Del	D0528g for	CTAGACCTTCACGATATCATATGGCTC	1021	D, 64411 - 65431
	D0528g rev	CAATGCACACCGATGAAGAACAG		
Der	D6512g for	GGTGTCTGGTTGAGGATAACCTAG	1064	D, 620145 - 621208
	D6512g rev	CCACTGAAAGGAGACGACAGTACAG		
Der2	D06556g for	GAAGTTGACCACTCTGCTGAGAAC	1075	D, 623962 - 625036
	D06556g rev	CGTTCTCGGTACTCAAGTCCTCG		
Dcl	D05808g for	CGCACAATGTACACAGATGTGG	1083	D, 553003 - 554086
	D05808g rev	CGGTCACTAGGATGGTTGC		
Em	E03542g for	AAATGGTACTAAACCACTGGACATCG	1024	E, 327315 - 328338
	E03542g rev	AGGTATCACTCAGTTGGCTTCAAG		
Em2	E02035g for	GAAGATCTGGATTGGCATCCAC	982	E, 201449 - 202431
	E02035g rev	CCTGATGCGTTGATGCAGTAAGC		
Em3	E02321g for	GACCACATACCAATGCAGTGAAG	1080	E, 223087 - 224166
	E02321g rev	CATGATGGCACATGCTATGCACC		
Em5	E01111g for	GACAAAGCCTTCAAGCAGGAC	1004	E, 101978 - 102981
	E01111g rev	GTAATGAGACAAGGCTTCATGCC		
Em6	E02695g for	CTGAAGGGAACGTGAGGAACAAGC	1085	E, 256068 - 257152
	E02695g rev	GCACTGCTCTAACCATCCAAAGG		
Em7	E02805g for	CCATGGTTCTCACACCATGAGG	1043	E, 266599 - 267641
	E02805g rev	CCATTGGGATTCCAAGCCATATCTG		
Em9	E00781g for	CTACCAGCAGTACCAAGCAGTTTC	983	E, 70475 - 71457
	E00781g rev	CATCAGCTTGAGAGGGACCCAC		
E75	E00847g for	CTATCGCTAATGCAGCTTC	1005	E, 75060 - 76064
	E00847g rev	GTCACGTAGTGCATGACAATCG		
E82	E00891g for	GTGCTCAGGGAGACAAACATAAGC	979	E, 81939 - 82917
	E00891g rev	CCAGGTTAACAGATGACGAGATAGC		
E87	E00957g for	CACCGCAGTATCTGGCTAATAGC	1049	E, 86761 - 87809
	E00957g rev	GGTGGGTGCAAGAACCTATCATGG		
E81, (MPT4)	E00869g for	CTAGGTAACGACGTTGAGGACCC	794	E, 81080 - 80287
	E00869g rev	GATGGCAAGGAAGAAGTGTGATC		
E155	E01617g for	CAAGCCTGGCTCTCATCATC	984	E, 155544 - 156527
	E01617g rev	GTTGACCTCAGACGTCAATGCAG		
E167	E01683g for	CACGAGGAAGTTCACGACGAG	1029	E, 167705 - 166677
	E01683g rev	CACTGGTTGTCTGCTCTT		

Probe name	Primer name	Primer (5'-3')	Product size, bp	Chromosome position, bp
Eer	E06468g for E06468g rev	TCAAACGAATGTGGGCTAATAGTCC TATCAGAAGGACAAGCACCAAGTC	1017	E, 646858 - 647874
Eel	E00451g for E00451g rev	CGAATCGAACGCTAGGGACCAAG CACAGATAACATGCCAGTCACAGC	919	E, 42333 - 43251
Ecr, (Ecen)	Ecr for Ecr rev	CTTCGACACTGTTGAAGAGAGGC GCACATTATCTCCACTGTCACTCG	778	E, 245440 - 246217
Ecr2	E02651g for E02651g rev	CAACCAGAGGGATTGCCCTAC GGTTAACGGTTTCAGCAGGGAG	1038	E, 251998 - 253035
Ecr3	E02585g for E02585g rev	CTCTGTTGACAACAGTGAAAGCC CAACGGAAATAGGGTCAACAGGAC	1038	E, 246602 - 247639
Ec40	E02959g for E02959g rev	GTCCGACGAACTTATGCCACAATG GCTACGGTTGACAACAGTCAAGC	1036	E, 281017 - 282052
PLB3	E02321g for E02321g rev	GCAGGTATACTGTCTGCATTGCAC GAAGATCCATCAGGCCATTGCAG	1028	E, 222799 - 223826
ACE2	E01331g for E01331g rev	CGATCTCGGTGATGAGCAATG CGTGGGCAGTATATCATTGGC	1012	E, 124493 - 125504
YPS4	E01749g for E01749g rev	GCTCGAAAACGGTGGCTCTTG GTCATCTGGCTTGATCTGC	1027	E, 173961 - 172935
YPS2	E01419g for E01419g rev	CAAGTTCCGTTGCATCGGCTTC TGTCCCTGCGAGTTCTCAAACC	670	E, 133034- 133733
YPS11	E01881g for E01881g rev	GTCAGCATTGGTAGTGACAAGCAG GTCTGAGCCAGTTGGAGCAAC	1023	E, 188193 - 189215
Fm	F03113g for F03113g rev	ACAGCAAGGTGCTAGTACTCCAG CCCATCGCTGTTATGATAGCATTC	945	F, 304285-305230
Fm2	F02541g for F02541g rev	GCCTACTTCATCTTACGACTCAAGC GATCACCAAGATGTATCTCACCAGC	1079	F, 248382 - 249460
Fm3	F01177g for F01177g rev	CTGGGAGAGCAAGGTACAATC CGGAGTTAGAGCACCAACAC	1062	F, 121101-122162
Fm4	F03531g for F03531g rev	CAGCCATGTTGAAACTGGCTTCG GTGGAGGAGTTGACCCACATTG	1026	F, 345523 - 346548
Fm5	F00671g for F00671g rev	CAACGCAATGTTACCAACGGTACAG GGAACGCCATGTGTCTTACACC	962	F, 74323 - 75284
Fm6, (SIZ1)	F02783g for F02783g rev	CTCCCGAGCATGATGGAATTGAC CCTCATCACTACAGTCCGACTGG	1024	F, 272086 - 273109
F78 (MYO2)	F00671g for F00671g rev	GATCTGAAAGACGGCACGTACC GTCAATACCAAGCAGTCAGCAG	1047	F, 78515 - 77469
F83	F00737g for F00737g rev	GAAGTTGGGTCTCTGTGAAGC CCTGATCTCCACCAAGACAACG	1086	F, 82844 - 83929
F80	F00693g for F00693g rev	CGTGTGGCTGTAATGTGTTGAAG CTTGTCAAAGTCACCATCCTTGGC	945	F, 79357 - 80301
F98	F00913g for F00913g rev	CTCCTATGTGGATCTCAAAGGCC CCAGGGATGTTGATCAGAACAGG	1036	F, 97193 - 98228
F254	F02607g for F02607g rev	CAGTGCCATGGAGTTAAGTGG GGACATAATGGTCTGATGAGTC	1071	F, 254879 - 253809
F270	F02739g for F02739g rev	GGACGCTGGTGGTACCTATAGG CGACATCGATATTAGCCTCGAGGG	1068	F, 270064 - 268997
F287	F02959g for F02959g rev	CCTCTTGTCAAGGCAGAGC CAAGCTTGTCTCTGCAACAAAC	1005	F, 286440 - 287444
Fel	F0253g for F0253g rev	TGCAGATGTCACAGTTTCCGTAATG CCACTAACGGTCCATACCAATG	1100	F, 31395-32494
Fer	F9053g for F9053g rev	GGATTGCAAGTTCTGGCTGGAAAC CATCGATTAACAGTCCCATTGGG	1029	F, 889821 - 890849
Fcl	F02277g for F02277g rev	CAGGCTTGTATGAGAACATGAGCAG CGCATAGGTATCCCTGGCATC	1037	F, 222424 - 223460
PDH1	F02717g for F02717g rev	CACCGATGACTCTAGTGTCTCG GCAATGTGCTGTGCTTCAG	1063	F, 261368 - 262430
AUS1	F01419g for F01419g rev	CCTAACGCATCGGTGACATTG GATCTAGGTCTCGGAAGAACCTG	913	F, 146789 - 145877
Gm	G05071g for G05071g rev	ATGGTAGTACTGTGAGCGACTACAAG GTAGGACCAATAGCACCAATAGAATGTG	1027	G, 481567-482593
Gm2	G01056g for G01056g rev	GTGCTCATCGATCTCGCAGAAC GGTTAGTGGCATATGTGATCCTC	1027	G, 100027 - 101053
Ger	G09911g for G09911g rev	TAACGGTGTGTTGCTTGTGGAAC ACCTGAATCGATATCGTGTGATCTG	901	G, 947151-948051

Probe name	Primer name	Primer (5'-3')	Product size, bp	Chromosome position, bp
Gel	G00374g for G00374g rev	GGCAGACTTGTACCAACAAAGAG CAATAGGAGCCTCTGGGATGACTAAC	1067	G, 37451–38517
Hm	H05621g for H05621g rev	CTGTTATTATCCTGGCAGTAACGATACC ATTGCTCTAGCTGAAAGATCTTCTG	982	H, 556628 - 557578
Hel	H0396g for H0396g rev	AATCGTGCCTAACTCCGAAGAG GCAGTACCGATAGTATTCCAGGATGTG	992	H, 38770 - 39761
Her	H10428g for H10428g rev	GCGTGGATAGTATGGCAGAAACG GATAACTCTGCAAAGGCAGCCG	1006	H, 1016984–1017989
Hcl	H09746g for H09746g rev	GCACAGCTAGTTAATGCACTTCCAG CTCTGAATGCTCTACCGTTGGAAAG	988	H, 952005 - 952992
Im	I05632g for I05632g rev	CTCGCAGTGAAGAAGTTGATCTACTC TGAATTGTCAGGAAACCTGGTC	1049	I, 531373 - 532421
Im2	I07821g for I07821g rev	GCAATTGGACAATCTGCGAACACG GGAGACTGTACACCAGTGAGATAGG	985	I, 753245 - 754229
Im3	I01628g for I01628g rev	CTACCGAATGCAGAGCGTGAATT CTACCTTGTAAATGGGCCACTTTG	997	I, 133412–134408
Ier	I10560g for I10560g rev	CATCCACTCACTTGGTATCTGCTT GTCTTCAAGCTGTTAGAGCCAACATC	970	I, 1033119–1034086
Iel	I0506g for I0506g rev	CAGGCTCTTGTATCGCATGG GCAGTCCCATGAGGTTATTGATG	1007	I, 38708–39714
Iel2	I00484g for I00484g rev	CTGTAAGTGCCTGGCTAACG CTCGTTGTTAGCACATGATCCGATG	1085	I, 35116 - 36200
Jm	J06270g for J06270g rev	AGAAGGGTAACACGTCACACTACTG GAGCTGTACAGACAGCTGTATAATCG	1076	J, 596032 - 597108
Jm2	J02530g for J02530g rev	GTGCTTGGCGATGATAAGACCAAG CTTGGCTTGTTCACCTTGTCC	975	J, 248631 - 249605
Jel	J0407g for J0407g rev	GGAACTACCGATGATAGTACATCATC GCAAATATAGTACCTGCACTTGGA	1077	J, 31334 - 32326
Jer	J11858g for J11858g rev	CACGTCACTCTGTTACAAAGAAGCC GTTGACCCAAGGAGACATTGAC	985	J, 1156557 - 1157541
Km	K05335g for K05335g rev	GTTGATCTCCTCAGTGCACGATT GTACGATTGATCATGGCTCCAGTC	926	K, 521154 - 522079
Ker	K13002g for K13002g rev	CCATTGAGCCATCTCTATCATTGAC CAACGCTACTAGCAGTAACAGTTG	1636	K, 1291094 - 1292729
Kel	K0319g for K0319g rev	AGTTCTGCAGGATCTTCAACACAG GATCCGGAATGACTCTAATGAGTC	986	K, 33655–34640
Kcr	K02937g for K02937g rev	CAGTAACTGCAGCAGTGAATATCAC TTGATCTGGCATACCAATTCTGGTC	1005	K, 260558 - 261561
Lm	L06644g for L06644g rev	GAGACAGATAGACGATCCTGGGTTAG CCTTGTCTTGGATGTCGGTATC	890	L, 748420 - 749309
Lm2	L02123g for L02123g rev	GACATCAACAGCTGTTGATGCGAG CGGGTGAATAGAAGTTCTACCAGC	1014	L, 248208 - 249221
Lm3	L03498g for L03498g rev	GTCAAGTGCAGTCAGTCC CAGTAGATACTCTGCTGATCAGCAGG	926	L, 399028–399953
Lel	L00297g for L00297g rev	GCACCTGGAATATGTCACATTGACAG CTTTCTGTTGGTAGCATCTGGTC	1233	L, 30628 - 31858
Ler	L13134g for L13134g rev	GAACTAGAGTGTAGCTGATTCCAACG AGTTTATGAACACGCACTTCTGG	1019	L, 1404234–1405252
Lcr	L09130g for L09130g rev	GCACATCCCTCAGAACATCCAGC GCGTCATCTCATGTCAGCTC	1018	L, 990366 - 991383
Mm	M06545g for M06545g rev	GGAGATGGTAGTAGACGTTGATCTTG GTTCAATTGCTGGATCTCGAG	832	M, 677469–678300
Mm3	M06413g for M06413g rev	GCTTCTATGCTCAGGCACTGTATC GCGAATCAATGCTGGAACCTACG	1081	M, 665997–666020
Mer	M13783g for M13783g rev	GGAGAATAGATAAAATGGTCCGAAC TCTTGTGCTTGATAACTGATTCTCAC	990	M, 1352772 - 1353762
Mel	M0286g for M0286g rev	CGATAAGTTGGTGACGCTAACGAC CTCAATGAAACGCTGTGCTGGATT	1215	M, 33677 - 34891
Mcr	M10527g for M10527g rev	CAAGGTGCCGTGAAATGGCTAC CAACGTCAAGGAGCAGTAACAGC	1026	M, 1052528–1053553
LSU rDNA	NL1 NL4	GCATATCAATAAGCGGAGGAAAAG GGTCCTGTTCAAGACGG	624	Multi-gene probe

**Table S4. Chromosomal rearrangements in the *C. glabrata* clinical isolates as shown in Fig.1**

Strain	Rearrangement
Y612	Translocation of the left arm of chromosome I onto chromosome L*
Y613	Translocation of the left arm of chromosome I onto chromosome L*
Y614	No detectable events
Y615	Translocation of the left arm of chromosome I onto chromosome L*
Y616	Translocation of the left arm of chromosome I onto chromosome L*
Y617	Translocation of the left arm of chromosome I onto chromosome L*
Y618	No detectable events
Y619	Translocation of the left arm of chromosome I onto chromosome L*
Y620	Translocation of the left arm of chromosome I onto chromosome L*
Y621	Translocation of the left arm of chromosome I onto chromosome L*, translocation of the left arm of chromosome L onto chromosome F, translocation of the right arm of chromosome G onto chromosome L, chromosomal duplication of the left chromosomal arm of chromosome E and its translocation onto chromosome G
Y622	Fusion of chromosome E and D, internal deletion within the CEN E region of the fusion chromosome D + E (further described in Fig. 3C), chromosomal duplication of the right chromosomal arm of chromosome D and its translocation onto chromosome B, chromosomal duplication of the left chromosomal arm of chromosome F and its translocation onto chromosome J, duplication of the left chromosomal arm of chromosome E and its fusion to the duplicated left arm of chromosome M
Y623	Translocation of the left arm of chromosome I onto chromosome L*
Y624	Translocation of the left arm of chromosome I onto chromosome L*, appearance of a novel chromosome composed of a large segmental duplication of chromosome E, internal deletion of the novel chromosome (further details are in Fig. 3A)
Y625	Translocation of the left arm of chromosome I onto chromosome L*
Y626	Translocation of a large segment of chromosome D onto L (in all strains but Y626, Y641, Y646, CBS 138 chromosome D has a different configuration and therefore it is likely that CBS 138-like chromosome D originated only in this branch by a translocation event)
Y627	No detectable events
Y640	No detectable events
Y641	Translocation of a large segment of chromosome D onto L (in all strains but Y626, Y641, Y646, CBS 138 chromosome D has a different configuration and therefore it is likely that CBS 138-like chromosome D originated only in this branch by a translocation event), reciprocal translocation between the left arm of chromosome K and the right arm of chromosome J
Y643	Translocation of the left arm of chromosome I onto chromosome L*
Y644	Translocation of the left arm of chromosome I onto chromosome L*
Y645	Reciprocal translocation between the right arm of chromosome M and the right arm of chromosome F
Y646	Translocation of a large segment of chromosome D onto L (in all strains but Y626, Y641, Y646, CBS 138 chromosome D has a different configuration and therefore it is likely that CBS 138-like chromosome D originated only in this branch by a translocation event)
Y647	Reciprocal translocation between the right arm of chromosome J and the right arm of chromosome E, chromosomal duplication of the left chromosomal arm of chromosome I and its translocation onto chromosome D
Y648	Translocation of the left arm of chromosome I onto chromosome L*
Y649	Reciprocal translocation between the right arm of chromosome G and the left arm of chromosome D
Y650	Reciprocal translocation between the right arm of chromosome M and the right arm of chromosome F
Y651	Translocation of the left arm of chromosome I onto chromosome L*, translocation of the left arm of chromosome L onto chromosome F
Y653	Translocation of the left arm of chromosome I onto chromosome L*
Y654	Translocation of the left arm of chromosome I onto chromosome L*
Y655	Translocation of the left arm of chromosome I onto chromosome L*, reciprocal translocation between the right arm of chromosome K and the right arm of chromosome A
Y656	Translocation of the left arm of chromosome I onto chromosome L*
Y659	Reciprocal translocation between the right arm of chromosome H and the left arm of chromosome L
Y660	Reciprocal translocation between the right arm of chromosome H and the left arm of chromosome L
Y661	Reciprocal translocation between the right arm of chromosome H and the left arm of chromosome L
Y662	Reciprocal translocation between the right arm of chromosome H and the left arm of chromosome L
Y663	Translocation of the left arm of chromosome I onto chromosome L*, appearance of a novel chromosome composed of a large segmental duplication of chromosome F
Y664	Translocation of the left arm of chromosome I onto chromosome L*, reciprocal translocation between the left arm of chromosome L and the left arm of chromosome M
Y665	Translocation of the left arm of chromosome I onto chromosome L*, the chromosomes E and C did not move into the gel in the electrophoretic field (chromosome circularization could explain such a retarded movement)
Y666	No detectable events
Y667	No detectable events
CBS 138	Translocation of a large segment of chromosome D onto L (in all strains but Y626, Y641, Y646, CBS 138 chromosome D has a different configuration and therefore it is likely that CBS 138-like chromosome D originated only in this branch by a translocation event)

The chromosome nomenclature of the sequenced strain CBS 138 is used.

\*Note that translocation of a large segment of chromosome L onto I is equally probable in the strains: Y614, Y618, Y622, Y626, Y627, Y640, Y641, Y645, Y646, Y647, Y649, Y650, Y659, Y660, Y661, Y662, Y666, Y667 and CBS 138.

**Table S5. Deletions within the analyzed *C. glabrata* chromosomes and possible breakpoint fragile sites**

Strain number	Rearrangement	Breakpoint mapping interval	Possible fragile sites
Y622	Internal deletion within the CEN E region of the chromosome D + E	(A) CAGL0E02035 g - CAGL0E02321 g (B) CAGL0E02805 g - CAGL0E02959 g	tRNA Gly gene, minisatellite (MS 21) ND
Y624	Internal deletion of the novel chromosome	(C) CAGL0E01419 g - CAGL0E01617 g (D) CAGL0E01881 g - CAGL0E02035 g	Megasatellite (MS 208) in the vicinity
Y624	Terminal deletion (left) of the novel chromosome	(E) CAGL0E00847 g - CAGL0E00869 g	ND
	Terminal deletion (right) of the novel chromosome	(F) CAGL0E02563 s - CAGL0E02585 g	Associated with centromere E
Y663	Terminal deletion (left) of the novel chromosome	(G) CAGL0F00671 g	ND
	Terminal deletion (right) of the novel chromosome	(H) CAGL0F02783 g - CAGL0F02915 g	ND

We mapped the putative breakpoints of 2 internal deletions and 4 terminal deletions within relatively short chromosomal intervals (2–20 kb). Several breakpoint intervals coincided with the breakpoints that occurred during the yeast evolutionary history and generated modern chromosomes in different lineages. These breakpoints were deduced from chromosomal alignments of Hemiascomycete yeasts (1, 2) (see Figs. S3 and S4). Within the *C. glabrata* breakpoint intervals, tRNA gene, satellites, nonsyntenic homologs, or centromere sequence can be found. This is consistent with the previous studies that showed that chromosomal region comprised of multiple tRNAs (3), centromere (4) minisatellites/megasatellites (5, 6), and Ty elements (7, 8), where the replication fork stalling occurs frequently, are a source of genomic rearrangements. Recently, Thierry et al. (6) reported that the genome of *C. glabrata* contains satellites. The absence of Ty elements at such sites may be explained by a limited number of transposable elements in the *C. glabrata* genome (only mutated copy of the Ty3 element remained) (9). Using nucleic acid dot plots (10), we did not identify any regions of significant identity within the breakpoint intervals of the internal deletions. This observation is consistent with the analysis of the breakpoint identities from *S. cerevisiae* where only short regions of sequence identity were involved in genome rearrangements (11, 12). ND, cannot be determined.

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